Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:27:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081126.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	`/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3081126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081126.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:27:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,948,358
Mapped reads	1,799,806 / 92.38%
Unmapped reads	148,552 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,062 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	63,337 / 3.25%
Duplication rate	2.97%
Clipped reads	691,771 / 35.51%

2.2. ACGT Content

Number/percentage of A's	34,211,383 / 27.91%
Number/percentage of C's	23,188,472 / 18.92%
Number/percentage of T's	38,346,225 / 31.28%
Number/percentage of G's	26,835,636 / 21.89%
Number/percentage of N's	1,411 / 0%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.2927

2.4. Mapping Quality

Mean Mapping Quality	46.8

2.5. Mismatches and indels

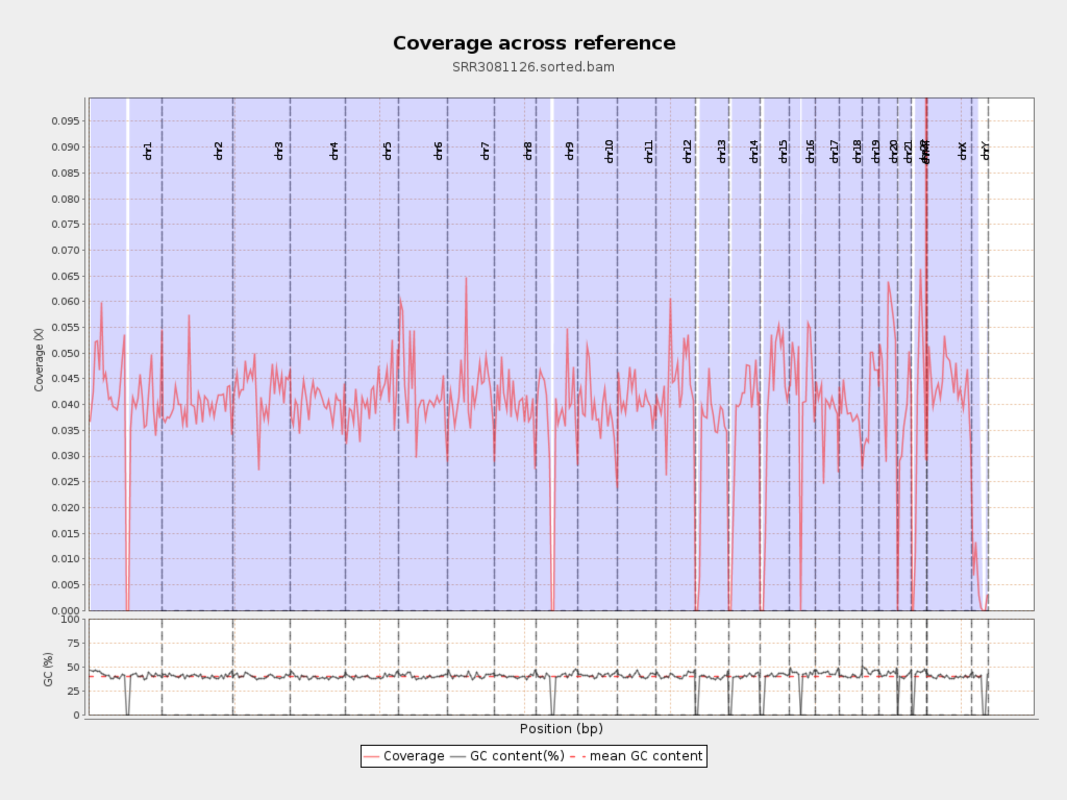
General error rate	0.83%
Mismatches	1,004,179
Insertions	8,778
Mapped reads with at least one insertion	0.48%
Deletions	26,200
Mapped reads with at least one deletion	1.44%
Homopolymer indels	48.79%

2.6. Chromosome stats

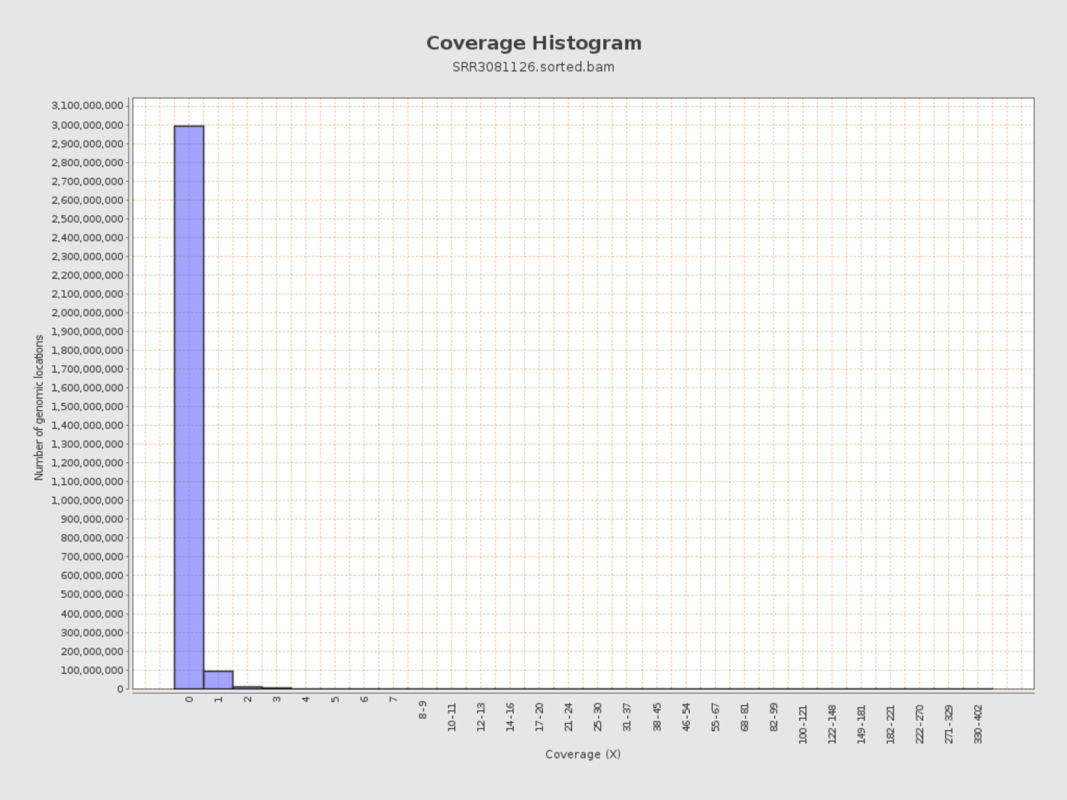
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10026601	0.0402	0.4021
chr2	243199373	9731691	0.04	0.3197
chr3	198022430	8473653	0.0428	0.232
chr4	191154276	7671000	0.0401	0.2329
chr5	180915260	7392887	0.0409	0.2277
chr6	171115067	7333501	0.0429	0.2647
chr7	159138663	6845485	0.043	0.4572

chr8	146364022	5844324	0.0399	0.3002
chr9	141213431	5170956	0.0366	0.2755
chr10	135534747	5314151	0.0392	0.2698
chr11	135006516	5513149	0.0408	0.2944
chr12	133851895	5887259	0.044	0.2379
chr13	115169878	3635602	0.0316	0.1983
chr14	107349540	3810917	0.0355	0.2221
chr15	102531392	3920234	0.0382	0.225
chr16	90354753	3856978	0.0427	0.2514
chr17	81195210	3143606	0.0387	0.2421
chr18	78077248	3010783	0.0386	0.4978
chr19	59128983	2425745	0.041	0.3332
chr20	63025520	3111204	0.0494	0.256
chr21	48129895	1643537	0.0341	0.2188
chr22	51304566	1725239	0.0336	0.2071
chrMT	16571	52216	3.151	2.4973
chrX	155270560	6809655	0.0439	0.2562
chrY	59373566	278335	0.0047	0.1052

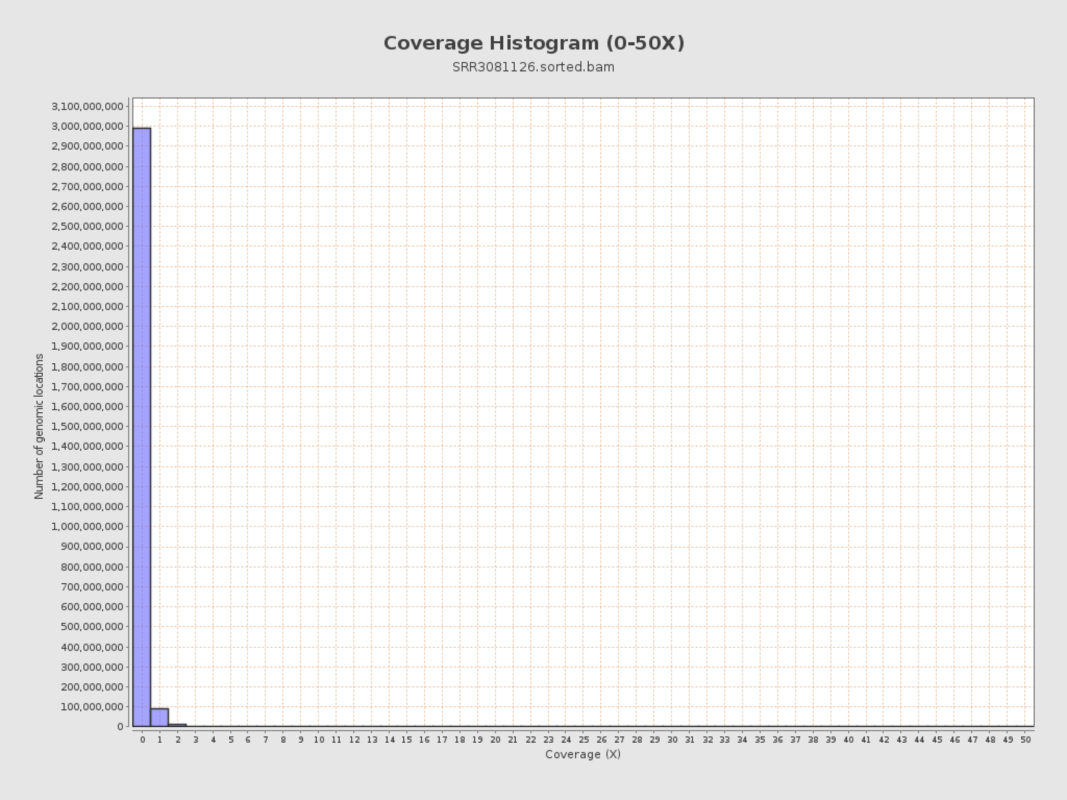
3. Results : Coverage across reference



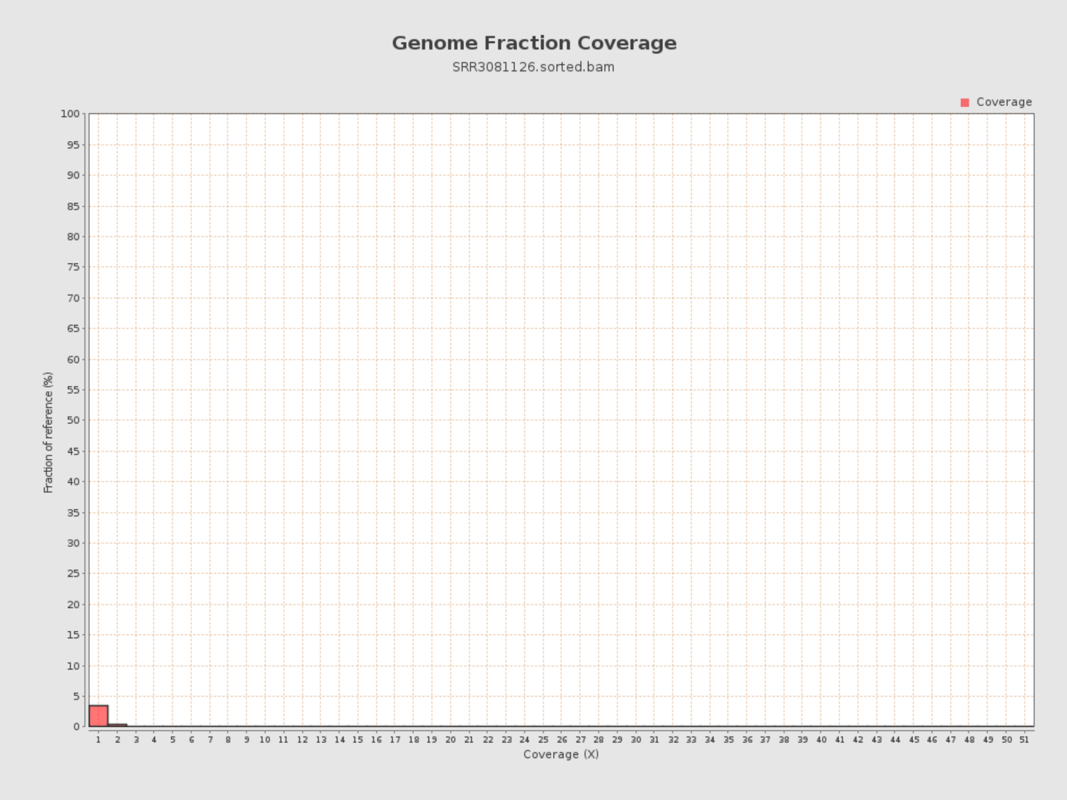
4. Results : Coverage Histogram



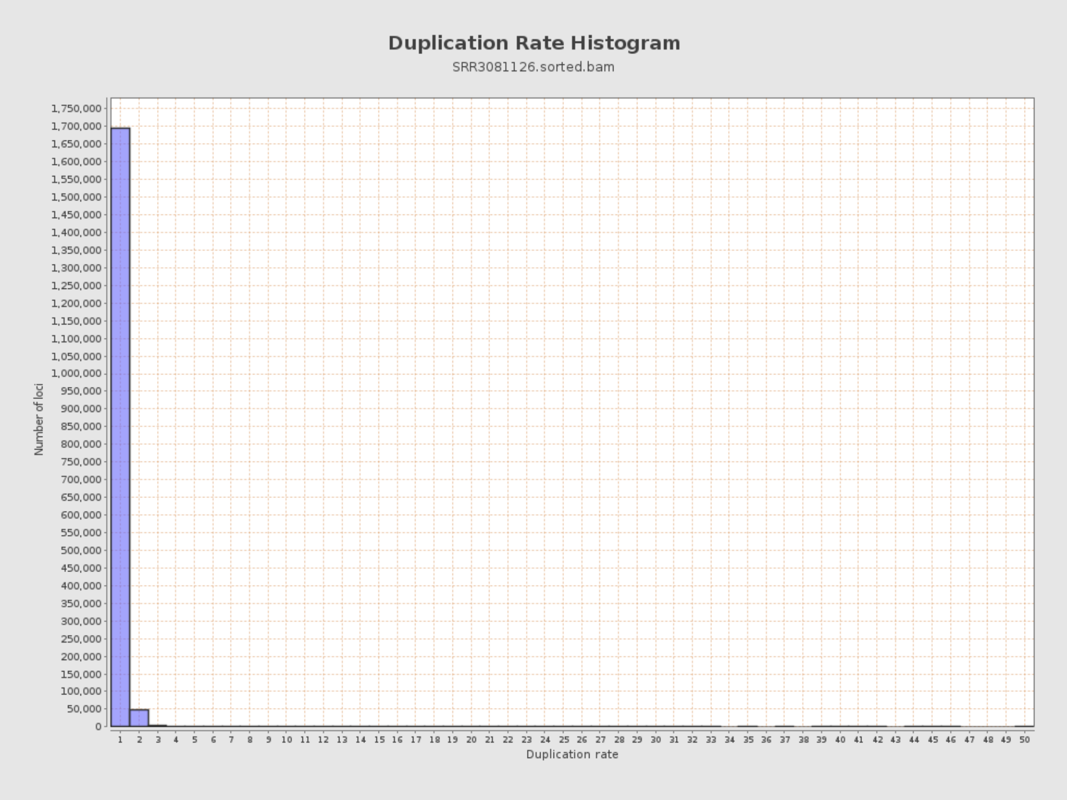
5. Results : Coverage Histogram (0-50X)



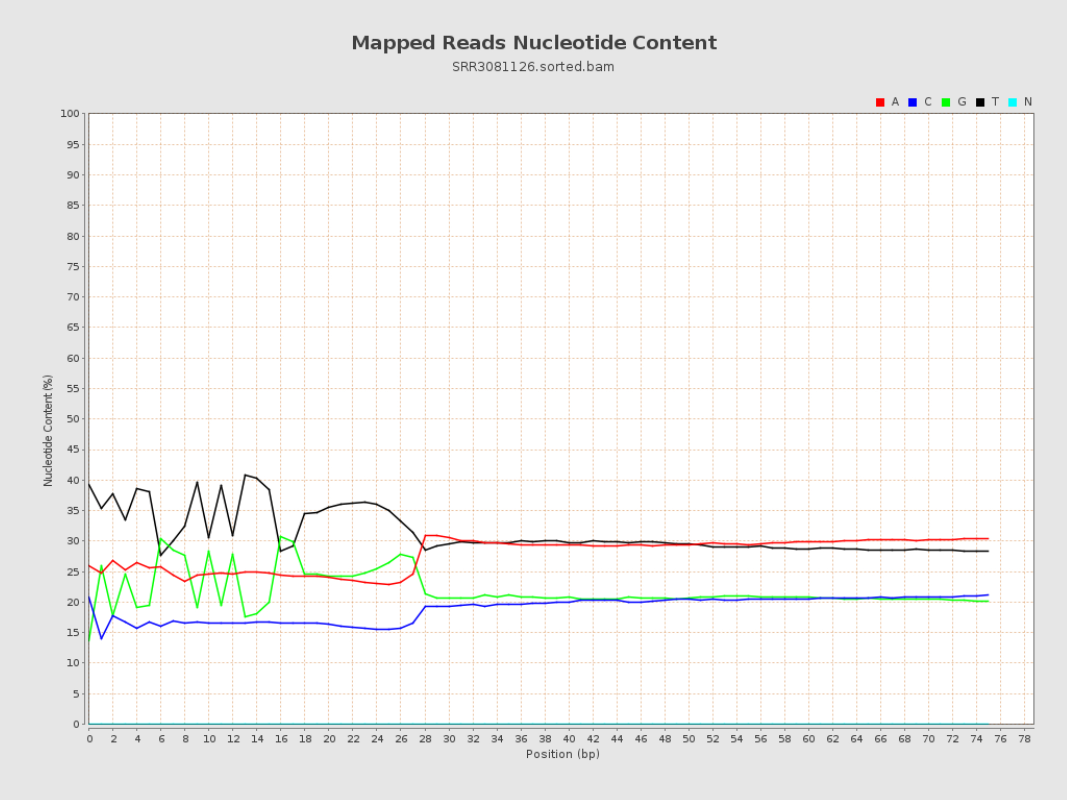
6. Results : Genome Fraction Coverage



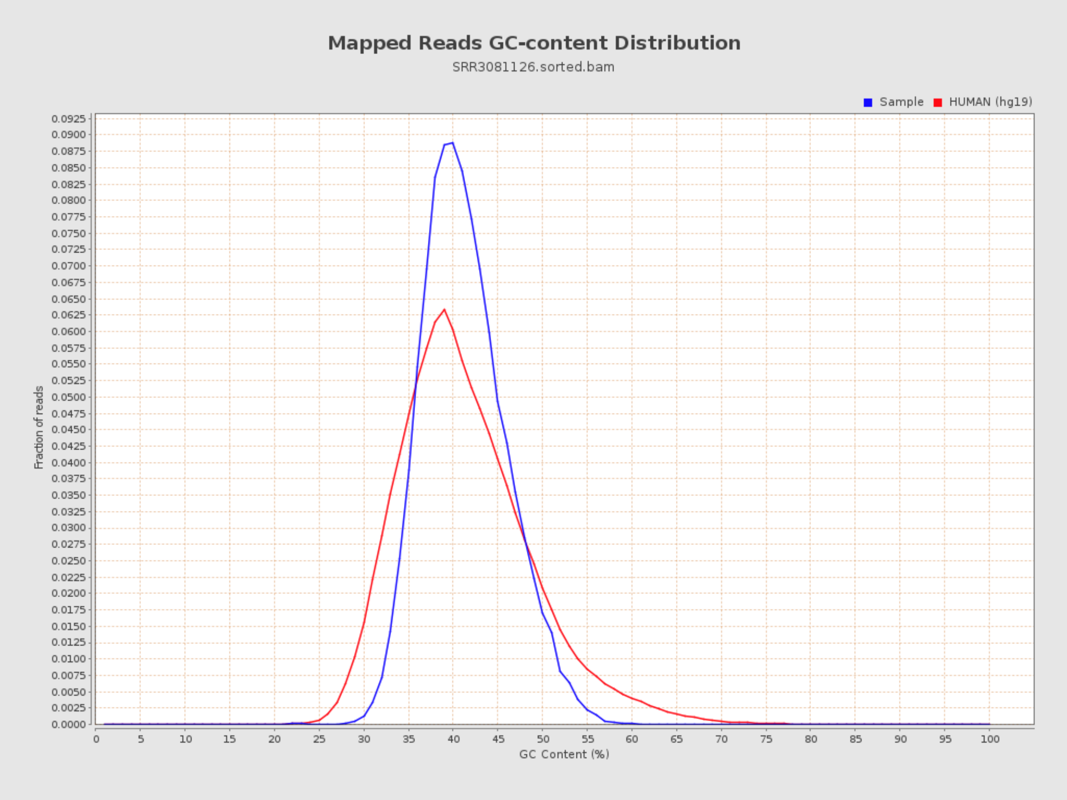
7. Results : Duplication Rate Histogram



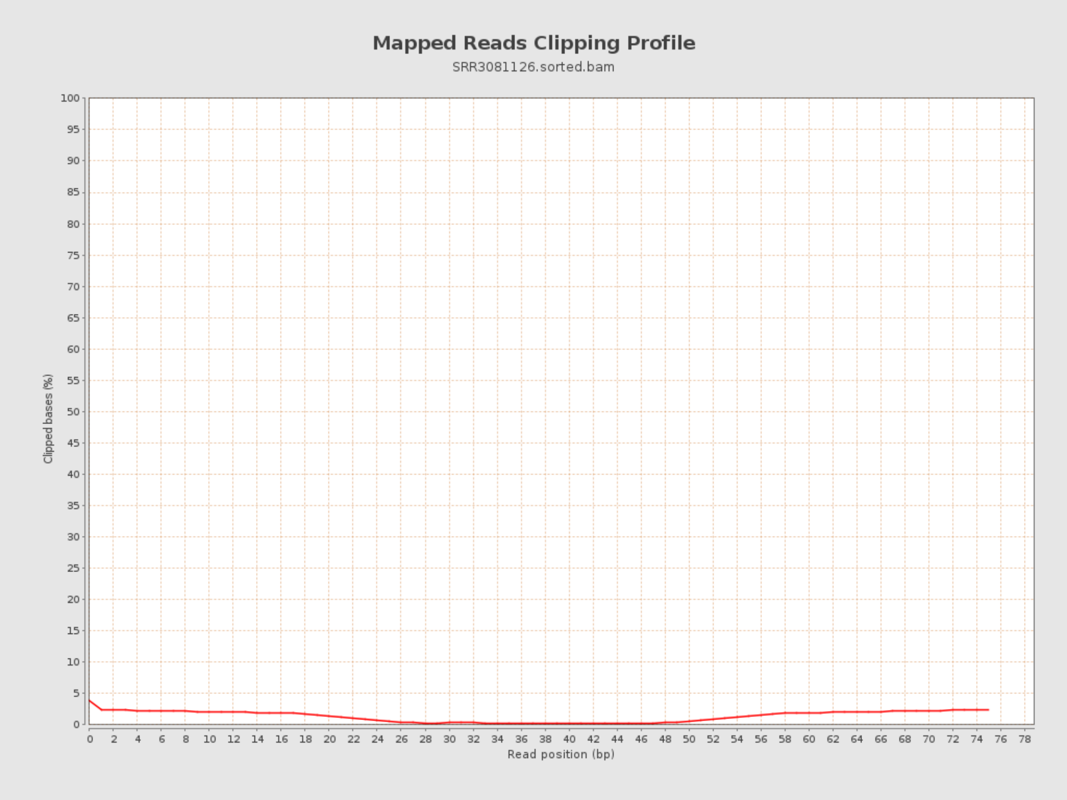
8. Results : Mapped Reads Nucleotide Content



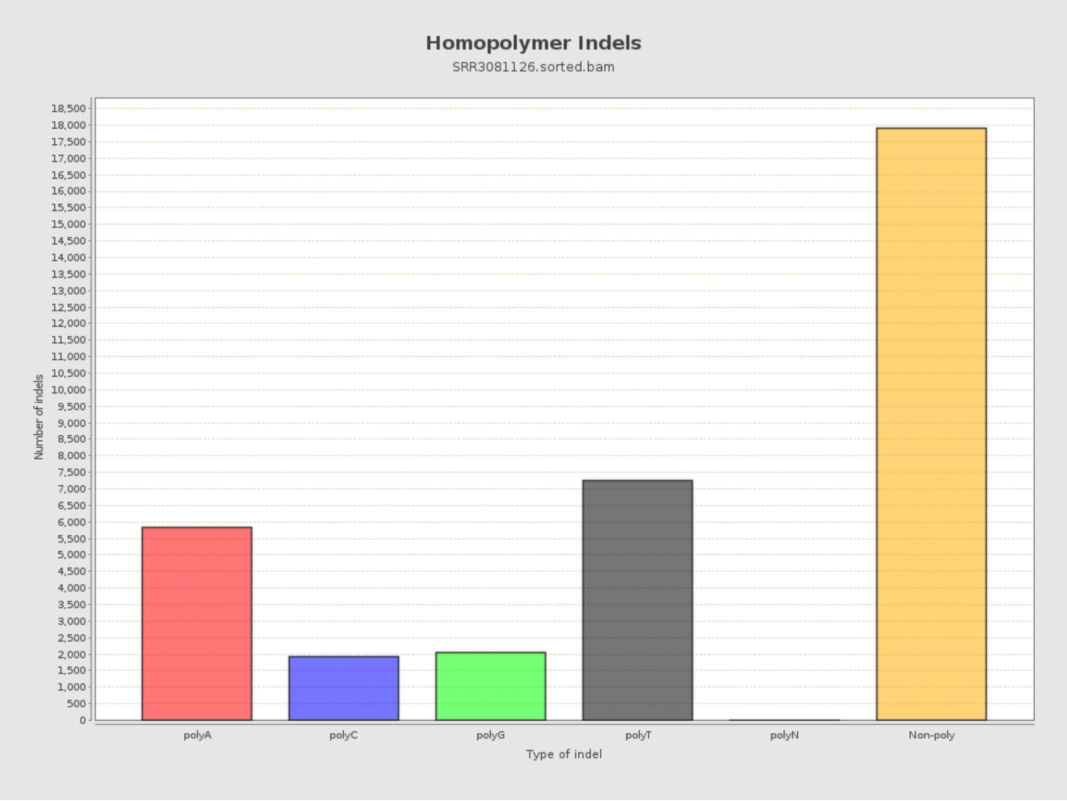
9. Results : Mapped Reads GC-content Distribution



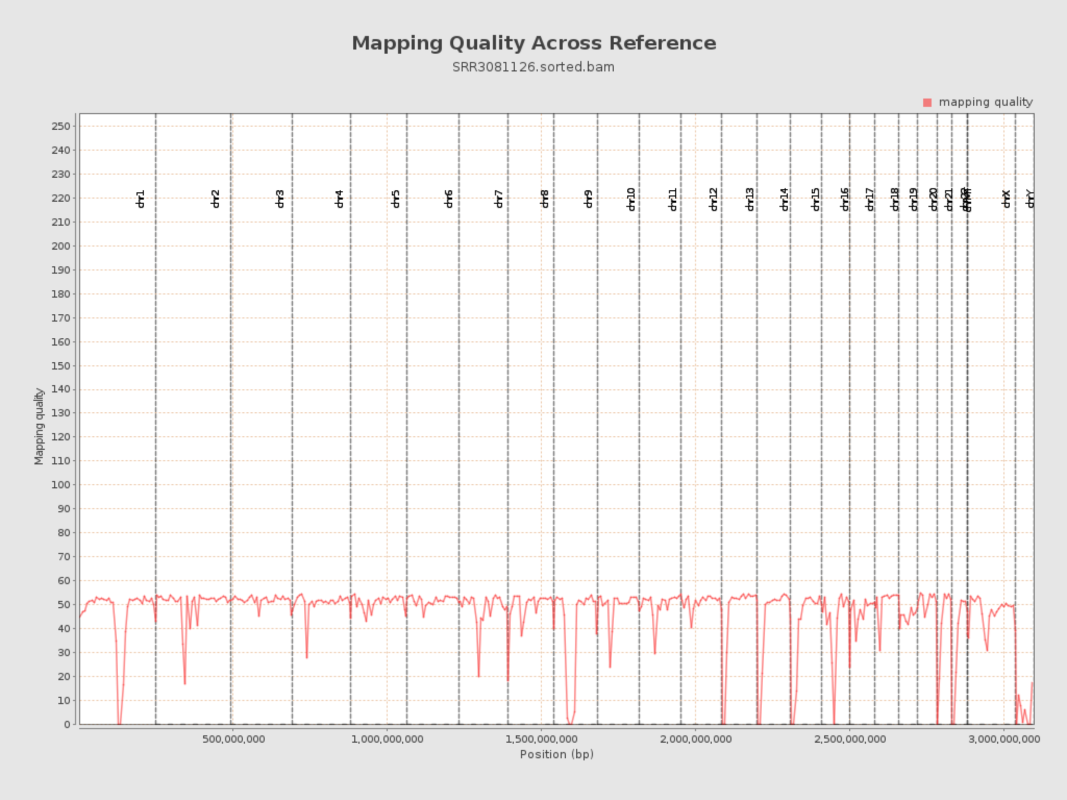
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram